Andrea Ganna

List of Publications by Year
in descending order

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64 papers	13,342 citations	109321 35 h-index	106344 65 g-index
85 all docs	85 docs citations	85 times ranked	29750 citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
2	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
3	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
4	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
5	Exploring Comorbidity Within Mental Disorders Among a Danish National Population. JAMA Psychiatry, 2019, 76, 259.	11.0	374
6	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
7	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	27.8	326
8	5 year mortality predictors in 498â€ˆ103 UK Biobank participants: a prospective population-based study. Lancet, The, 2015, 386, 533-540.	13.7	319
9	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. ELife, 2019, 8, .	6.0	276
10	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. Science, 2019, 365, .	12.6	245
11	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
12	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
13	Large-scale Metabolomic Profiling Identifies Novel Biomarkers for Incident Coronary Heart Disease. PLoS Genetics, 2014, 10, e1004801.	3.5	225
14	Multilocus Genetic Risk Scores for Coronary Heart Disease Prediction. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2267-2272.	2.4	138
15	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. Nature Genetics, 2018, 50, 1600-1607.	21.4	132
16	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	21.4	124
17	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	30.7	109
18	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	6.2	102

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19	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	14.8	90
20	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
21	Gene Ã— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. Human Molecular Genetics, 2015, 24, 4728-4738.	2.9	84
22	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	12.8	79
23	Risk Prediction Measures for Case-Cohort and Nested Case-Control Designs: An Application to Cardiovascular Disease. American Journal of Epidemiology, 2012, 175, 715-724.	3.4	75
24	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19. Nature Genetics, 2022, 54, 125-127.	21.4	75
25	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. Journal of Clinical Investigation, 2021, 131, .	8.2	72
26	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	3.5	66
27	The human genetic epidemiology of COVID-19. Nature Reviews Genetics, 2022, 23, 533-546.	16.3	64
28	The metabolic fingerprint of p,pâ€²-DDE and HCB exposure in humans. Environment International, 2016, 88, 60-66.	10.0	61
29	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. Human Molecular Genetics, 2015, 24, 6849-6860.	2.9	55
30	Identification of metabolic profiles associated with human exposure to perfluoroalkyl substances. Journal of Exposure Science and Environmental Epidemiology, 2019, 29, 196-205.	3.9	55
31	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
32	Genetic predictors of testosterone and their associations with cardiovascular disease and risk factors: A Mendelian randomization investigation. International Journal of Cardiology, 2018, 267, 171-176.	1.7	49
33	Glucose challenge metabolomics implicates medium-chain acylcarnitines in insulin resistance. Scientific Reports, 2018, 8, 8691.	3.3	47
34	Detailed stratified GWAS analysis for severe COVID-19 in four European populations. Human Molecular Genetics, 2022, 31, 3945-3966.	2.9	46
35	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2021, 597, E3-E4.	27.8	45
36	Novel genes and sex differences in COVID-19 severity. Human Molecular Genetics, 2022, 31, 3789-3806.	2.9	38

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37	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	6.5	34
38	Genetic determinants of mortality. Can findings from genome-wide association studies explain variation in human mortality?. Human Genetics, 2013, 132, 553-561.	3.8	29
39	Large-scale non-targeted metabolomic profiling in three human population-based studies. Metabolomics, 2016, 12, 1.	3.0	29
40	The metabolites urobilin and sphingomyelin (30:1) are associated with incident heart failure in the general population. ESC Heart Failure, 2019, 6, 764-773.	3.1	23
41	Heterogeneous contribution of microdeletions in the development of common generalised and focal epilepsies. Journal of Medical Genetics, 2017, 54, 598-606.	3.2	22
42	Proteomic profiles before and during weight loss: Results from randomized trial of dietary intervention. Scientific Reports, 2020, 10, 7913.	3.3	22
43	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. Nature Communications, 2022, 13, .	12.8	22
44	Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study. PLoS Genetics, 2016, 12, e1006379.	3.5	20
45	Effects of cigarette smoking on cardiovascular-related protein profiles in two community-based cohort studies. Atherosclerosis, 2016, 254, 52-58.	0.8	18
46	The plasma protein profile and cardiovascular risk differ between intima-media thickness of the common carotid artery and the bulb: A meta-analysis and a longitudinal evaluation. Atherosclerosis, 2020, 295, 25-30.	0.8	18
47	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. Nature Aging, 2022, 2, 19-30.	11.6	17
48	A Multi-Cohort Metabolomics Analysis Discloses Sphingomyelin (32:1) Levels to be Inversely Related to Incident Ischemic Stroke. Journal of Stroke and Cerebrovascular Diseases, 2020, 29, 104476.	1.6	14
49	Effect of General Adiposity and Central Body Fat Distribution on the Circulating Metabolome: A Multicohort Nontargeted Metabolomics Observational and Mendelian Randomization Study. Diabetes, 2022, 71, 329-339.	0.6	14
50	Development and validation of risk prediction models for multiple cardiovascular diseases and Type 2 diabetes. PLoS ONE, 2020, 15, e0235758.	2.5	13
51	Discriminating bipolar depression from major depressive disorder with polygenic risk scores. Psychological Medicine, 2020, 51, 1-8.	4.5	12
52	Non-targeted urine metabolomics and associations with prevalent and incident type 2 diabetes. Scientific Reports, 2020, 10, 16474.	3.3	11
53	Fast estimation of genetic correlation for biobank-scale data. American Journal of Human Genetics, 2022, 109, 24-32.	6.2	11
54	Association Between Episodic Memory and Genetic Risk Factors for Alzheimer's Disease in South Asians from the Longitudinal Aging Study in Indiaâ€“Diagnostic Assessment of Dementia (LASIâ€ÐAD). Journal of the American Geriatrics Society, 2020, 68, S45-S53.	2.6	10

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55	Prediction impact curve is a new measure integrating intervention effects in the evaluation of risk models. Journal of Clinical Epidemiology, 2016, 69, 89-95.	5.0	8
56	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	2.5	6
57	Utilizing Twins as Controls for Non-Twin Case-Materials in Genome Wide Association Studies. PLoS ONE, 2013, 8, e83101.	2.5	6
58	Response to Comment on â€œLarge-scale GWAS reveals insights into the genetic architecture of same-sex sexual behaviorâ€. Science, 2021, 371, .	12.6	5
59	Genome studies must account for historyâ€”Response. Science, 2019, 366, 1461-1462.	12.6	4
60	Clinical Conditions and Their Impact on Utility of Genetic Scores for Prediction of Acute Coronary Syndrome. Circulation Genomic and Precision Medicine, 2021, 14, e003283.	3.6	4
61	Nonparametric estimation of the rediscovery rate. Statistics in Medicine, 2016, 35, 3203-3212.	1.6	2
62	Common and rare variants in Alzheimerâ€™s disease genes are associated with episodic memory in South Asians from the LASIâ€ÐAD study. Alzheimer's and Dementia, 2020, 16, e045189.	0.8	0
63	Polygenic risk score for general cognitive function is associated with measures of cognition in South Asians from the LASI-DAD Study.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053977.	0.8	0
64	Common and rare variants in topologically associated domains for cognitive function in South Asians from the LASI-DAD Study.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054029.	0.8	0